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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/005,675

DATE: 12/17/2001

TIME: 10:38:45

Input Set : A:\P0530P1C10.txt

Output Set: N:\CRF3\12172001\J005675.raw

## SEQUENCE LISTING

*delete duplicate*

## W--&gt; 3 SEQUENCE LISTING

## 5 (1) GENERAL INFORMATION:

7 (i) APPLICANT: Shak, Steven

9 (ii) TITLE OF INVENTION: Anti-Infective Therapy

11 (iii) NUMBER OF SEQUENCES: 25

13 (iv) CORRESPONDENCE ADDRESS:

14 (A) ADDRESSEE: Genentech, Inc.

15 (B) STREET: 1 DNA Way

16 (C) CITY: South San Francisco

17 (D) STATE: California

18 (E) COUNTRY: USA

19 (F) ZIP: 94080

21 (v) COMPUTER READABLE FORM:

22 (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

23 (B) COMPUTER: IBM PC compatible

24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

25 (D) SOFTWARE: WinPatin (Genentech)

27 (vi) CURRENT APPLICATION DATA:

C--&gt; 28 (A) APPLICATION NUMBER: US/10/005,675

C--&gt; 29 (B) FILING DATE: 07-Nov-2001

30 (C) CLASSIFICATION:

60 (vii) PRIOR APPLICATION DATA:

33 (A) APPLICATION NUMBER: 09/669306

34 (B) FILING DATE: 25-Sep-2001

37 (A) APPLICATION NUMBER: 08/873506

38 (B) FILING DATE: 08-Dec-1999

41 (A) APPLICATION NUMBER: 08/643195

42 (B) FILING DATE: 06-May-1996

45 (A) APPLICATION NUMBER: 08/459909

46 (B) FILING DATE: 02-Jun-1995

49 (A) APPLICATION NUMBER: 08/191749

50 (B) FILING DATE: 03-Feb-1994

53 (A) APPLICATION NUMBER: 07/914,226

54 (B) FILING DATE: 13-Jul-1992

57 (A) APPLICATION NUMBER: 07/448038

58 (B) FILING DATE: 08-Dec-1989

61 (A) APPLICATION NUMBER: 07/289958

62 (B) FILING DATE: 23-Dec-1988

64 (viii) ATTORNEY/AGENT INFORMATION:

65 (A) NAME: Johnston, Sean A.

66 (B) REGISTRATION NUMBER: 35,910

67 (C) REFERENCE/DOCKET NUMBER: P0530P1C10

69 (ix) TELECOMMUNICATION INFORMATION:

70 (A) TELEPHONE: 650/225-3562

71 (B) TELEFAX: 650/952-9881

72 (2) INFORMATION FOR SEQ ID NO: 1:

Does Not Comply  
Corrected Diskette Needed

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```

74      (i) SEQUENCE CHARACTERISTICS:
75          (A) LENGTH: 51 base pairs
76          (B) TYPE: Nucleic Acid
77          (C) STRANDEDNESS: Single
78          (D) TOPOLOGY: Linear
80      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
83      GTGCTGGACA CCTACCAGTA TGATGATGGC TGTGAGTCCT GTGGCAATGA 50
85      C 51
87      (2) INFORMATION FOR SEQ ID NO: 2:
89          (i) SEQUENCE CHARACTERISTICS:
90              (A) LENGTH: 17 amino acids
91              (B) TYPE: Amino Acid
92              (D) TOPOLOGY: Linear
94          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
96      Val Leu Asp Thr Tyr Gln Tyr Asp Asp Gly Cys Glu Ser Cys Gly
97          1             5             10             15
99      Asn Asp
102     (2) INFORMATION FOR SEQ ID NO: 3:
104         (i) SEQUENCE CHARACTERISTICS:
105             (A) LENGTH: 71 base pairs
106             (B) TYPE: Nucleic Acid
107             (C) STRANDEDNESS: Single
108             (D) TOPOLOGY: Linear
110         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
113      TATGACGTCT ACCTGGACGT GCAGCAGAAG TGGCATCTGA ATGATGTGAT 50
115      GCTGATGGGC GACTTCAACG C 71
117     (2) INFORMATION FOR SEQ ID NO: 4:
119         (i) SEQUENCE CHARACTERISTICS:
120             (A) LENGTH: 23 amino acids
121             (B) TYPE: Amino Acid
122             (D) TOPOLOGY: Linear
124         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
126      Tyr Asp Val Tyr Leu Asp Val Gln Gln Lys Trp His Leu Asn Asp
127          1             5             10             15
129      Val Met Leu Met Gly Asp Phe Asn
130          20
132     (2) INFORMATION FOR SEQ ID NO: 5:
134         (i) SEQUENCE CHARACTERISTICS:
135             (A) LENGTH: 42 base pairs
136             (B) TYPE: Nucleic Acid
137             (C) STRANDEDNESS: Single
138             (D) TOPOLOGY: Linear
140         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
143      CTGAAGATCG CAGCCTTCAA CATCCAGACA TTTGGGGAGA CC 42
145     (2) INFORMATION FOR SEQ ID NO: 6:
147         (i) SEQUENCE CHARACTERISTICS:
148             (A) LENGTH: 42 base pairs
149             (B) TYPE: Nucleic Acid
150             (C) STRANDEDNESS: Single

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151         (D) TOPOLOGY: Linear
153     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
156     TCCGCATGTC CCAGGGCCAC AGGCAGCGTT TCCTGGTAGG AC 42
158 (2) INFORMATION FOR SEQ ID NO: 7:
160     (i) SEQUENCE CHARACTERISTICS:
161         (A) LENGTH: 31 base pairs
162         (B) TYPE: Nucleic Acid
163         (C) STRANDEDNESS: Single
164         (D) TOPOLOGY: Linear
166     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
169     TTGAAGATCG CAGCCTTCAA CATCCAGACA T 31
171 (2) INFORMATION FOR SEQ ID NO: 8:
173     (i) SEQUENCE CHARACTERISTICS:
174         (A) LENGTH: 31 base pairs
175         (B) TYPE: Nucleic Acid
176         (C) STRANDEDNESS: Single
177         (D) TOPOLOGY: Linear
179     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
182     CTGGATGTTG AAGGVTGCGA TCTTCAATGC A 31
184 (2) INFORMATION FOR SEQ ID NO: 9:
186     (i) SEQUENCE CHARACTERISTICS:
187         (A) LENGTH: 42 base pairs
188         (B) TYPE: Nucleic Acid
189         (C) STRANDEDNESS: Single
190         (D) TOPOLOGY: Linear
192     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
195     CTAGAATTAT GTTAAAAATT GCAGCATTTA ATATTCAAAC AT 42
197 (2) INFORMATION FOR SEQ ID NO: 10:
199     (i) SEQUENCE CHARACTERISTICS:
200         (A) LENGTH: 34 base pairs
201         (B) TYPE: Nucleic Acid
202         (C) STRANDEDNESS: Single
203         (D) TOPOLOGY: Linear
205     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
208     TTGAATATTA AATGCTGCAA TTTTAAACAT AATT 34
210 (2) INFORMATION FOR SEQ ID NO: 11:
212     (i) SEQUENCE CHARACTERISTICS:
213         (A) LENGTH: 7 amino acids
214         (B) TYPE: Amino Acid
215         (D) TOPOLOGY: Linear
217     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
219     Met Leu Lys Ile Ala Ala Phe
220     1           5
222 (2) INFORMATION FOR SEQ ID NO: 12:
224     (i) SEQUENCE CHARACTERISTICS:
225         (A) LENGTH: 1039 base pairs
226         (B) TYPE: Nucleic Acid
227         (C) STRANDEDNESS: Double
228         (D) TOPOLOGY: Linear

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230 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

233 TCCTGCACAG GCAGTGCCTT GAAGTGCTTC TTCAGAGACC TTTCTTCATA 50

235 GACTACTTTT TTTTCTTTAA GCAGCAAAAG GAGAAAATTG TCATCAAAGG 100

237 ATATTCCAGA TTCTTGACAG CATTCTCGTC ATCTCTGAGG ACATCACCAT 150

239 CATCTCAGGA TGAGGGGCGAT GAAGCTGCTG GGGGCGCTGC TGGCACTGGC 200

241 GGCCCTACTG CAGGGGGGCGG TGTCCCTGAA GATCGCAGCC TTCAACATCC 250

243 AGACATTTGG GGAGACCAAG ATGTCCAATG CCACCCTCGT CAGCTACATT 300

245 GTGCAGATCC TGAGCCGCTA TGACATCGCC CTGGTCCAGG AGGTCAGAGA 350

247 CAGCCACCTG ACTGCCGTGG GGAAGCTGCT GGACAACCTC AATCAGGATG 400

249 CACCAGACAC CTATCACTAC GTGGTCAGTG AGCCACTGGG ACGGAACAGC 450

251 TATAAGGAGC GCTACCTGTT CGTGTACAGG CCTGACCAGG TGTCTGCGGT 500

253 GGACAGCTAC TACTACGATG ATGGCTGCGA GCCCTGCGGG AACGACACCT 550

255 TCAACCGAGA GCCAGCCATT GTCAGGTTCT TCTCCCGGTT CACAGAGGTC 600

257 AGGGAGTTTG CCATTGTTCC CCTGCATGCG GCCCCGGGGG ACGCAGTAGC 650

259 CGAGATCGAC GCTCTCTATG ACGTCTACCT GGATGTCCAA GAGAAATGGG 700

261 GCTTGGAGGA CGTCATGTTG ATGGGCGACT TCAATGCGGG CTGCAGCTAT 750

263 GTGAGACCCT CCCAGTGGTC ATCCATCCGC CTGTGGACAA GCCCCACCTT 800

265 CCAGTGGCTG ATCCCCGACA GCGCTGACAC CACAGCTACA CCCACGCACT 850

267 GTGCCTATGA CAGGATCGTG GTTGCAAGGA TGCTGCTCCG AGGCGCCGTT 900

269 GTTCCCGACT CGGCTCTTCC CTTTAACCTC CAGGCTGCCT ATGGCCTGAG 950

271 TGACCAACTG GCCCAAGCCA TCAGTGACCA CTATCCAGTG GAGGTGATGC 1000

273 TGAAGTGAGC AGCCCTCTCC CACACCAGTT GAACTGCAG 1039

275 (2) INFORMATION FOR SEQ ID NO: 13:

277 (i) SEQUENCE CHARACTERISTICS:

278 (A) LENGTH: 341 amino acids

279 (B) TYPE: Amino Acid

280 (D) TOPOLOGY: Linear

282 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

284 Ser Cys Thr Gly Ser Ala Leu Lys Cys Phe Phe Arg Asp Leu Ser

285 1 5 10 15

287 Ser Thr Thr Phe Phe Ser Leu Ser Ser Lys Arg Arg Lys Leu Ser

288 20 25 30

290 Ser Lys Asp Ile Pro Asp Ser Gln His Ser Arg His Leu Gly His

291 35 40 45

293 His His His Leu Arg Met Arg Gly Met Lys Leu Leu Gly Ala Leu

294 50 55 60

296 Leu Ala Leu Ala Ala Leu Leu Gln Gly Ala Val Ser Leu Lys Ile

297 65 70 75

299 Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu Thr Lys Met Ser Asn

300 80 85 90

302 Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu Ser Arg Tyr Asp

303 95 100 105

305 Ile Ala Leu Val Gln Glu Val Arg Asp Ser His Leu Thr Ala Val

306 110 115 120

308 Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala Pro Asp Thr Tyr

309 125 130 135

311 His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser Tyr Lys Glu

312 140 145 150

314 Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser Ala Val Asp

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315          155          160          165
317 Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp Thr
318          170          175          180
320 Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr
321          185          190          195
323 Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly
324          200          205          210
326 Asp Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp
327          215          220          225
329 Val Gln Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp
330          230          235          240
332 Phe Asn Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser
333          245          250          255
335 Ile Arg Leu Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp
336          260          265          270
338 Ser Ala Asp Thr Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg
339          275          280          285
341 Ile Val Val Ala Gly Met Leu Leu Arg Gly Ala Val Val Pro Asp
342          290          295          300
344 Ser Ala Leu Pro Phe Asn Phe Gln Ala Ala Tyr Gly Leu Ser Asp
345          305          310          315
347 Gln Leu Ala Gln Ala Ile Ser Asp His Tyr Pro Val Glu Val Met
348          320          325          330
350 Leu Lys Ala Ala Pro Pro His Thr Ser Thr Ala
351          335          340
353 (2) INFORMATION FOR SEQ ID NO: 14:
355     (i) SEQUENCE CHARACTERISTICS:
356         (A) LENGTH: 260 amino acids
357         (B) TYPE: Amino Acid
358         (D) TOPOLOGY: Linear
360     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:
362 Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu Thr Lys
363 1      5      10      15
365 Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu Ser
366      20      25      30
368 Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser His Leu
369      35      40      45
371 Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala Pro
372      50      55      60
374 Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser
375      65      70      75
377 Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser
378      80      85      90
380 Ala Val Asp Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly
381      95     100     105
383 Asn Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser
384     110     115     120
386 Arg Phe Thr Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala
387     125     130     135

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